

>AF249738 ACCESSION:AF249738 NID: gi 8571425 gb AF249738.1 AF249738
Mus musculus Pb99 gene sequence
Length = 2127

Score = 358 bits (910), Expect(3) = 0.0
Identities = 210/293 (72%), Positives = 233/293 (80%)
Frame = +1

Query: 206 RPPPNMTLTCVFDVTKGTTGDWSSEGCSTEVRPEGTVCCCDHLTFFALLLRPTLDQSTV 265
R P N+ LTCVFDW+ KG DW S CST TVC CDHLTFFALLLRP LD +T
Sbjct: 748 RSPHNVILTCVFDMAKG---DWDSH-CSTVPGDGRTVCRC DHLTFFALLLRPILDLATA 915
Query: 266 HILTRISQAGCGVSMIFLAFTIILYAFLRLSRERFKSEDAPKIHVALGGSLFLLNLAF LV 325
LTRISQAG VSMIFLAFT++LY R S +RFKSEDAPKIH+AL SLFLLNL FL
Sbjct: 916 QTLTRISQAGSAVSMIFLAFTMVLYVAFRFSLQRFKSEDAPKIHMAISISLFLNLTLFLI 1095
Query: 326 NVGSGSKGSDAACWARGAVFHYFLLCAFTWMGLEAFHLYLLAVRVFNTYFGHYFLKLSLV 385
NVGS S+G A+CW R A+FHYFLLC FTWMGLEAFHLYLLA+RVFNTYFGHYFLKLSL+
Sbjct: 1096 NVGSSSQGPPASCWVRAAIFHYFLLCVFTWMGLEAFHLYLLAIRVFNTYFGHYFLKLSLL 1275
Query: 386 GWGLPALMVIGTGSANSYGLYTIRDRENRTSLELCWFREGTTMYALYITVHGYFLITFLF 445
WGLP L+VIG GS+NSYG+YTIRD+ENRTSLELCWF++ ALY TVHGYFL+TFLF
Sbjct: 1276 AWGLPVLVIGAGSSNSYGVYTIRDQENRTSLELCWFQKEP---ALYATVHGYFLVTFLF 1446
Query: 446 GMVVLALVVKIFTLSRATAVKERKGNRKKVLTLLGLSSLVGVTWGLAIFTPL 498
G VVLALV WKIFTL TA K +G K VLT+LGLSSLVG+TWGLA+ TPL
Sbjct: 1447 GAVVLALVAWKIFTLPSVTAGKGQGPWKSVLTVLGLSSLVGMTWGLAVLTPL 1605

Score = 245 bits (618), Expect(3) = 0.0
Identities = 129/215 (60%), Positives = 159/215 (74%), Gaps = 2/215 (0%)
Frame = +2

Query: 1 MATPRGLGALLLLLLLLPTSGQEKPTGPRNTC--LGSNNMYDIFNLNDKALCFTKCRQSG 58
MAT R LG L LLL + E+ TE PRN C L + YD F+LND A CFTKC QS
Sbjct: 17 MATARSLGLLFFLLL---TSDEETTEEPRNVCRRQLQEGHEYDTFDLNDTAQCFTKCGQSE 187
Query: 59 SDSCNVENLQRYWLNYEAHLMKEGLTQKVNTPFKALVQNLSTNTAEDFYFSLEPSQVPR 118
C+V NLQRYWLNYE++L++ + + V+ PF+KAL+QN+ST+ +ED +SL SQ+PR
Sbjct: 188 HSPCDVGNLQRYWLNYESYLLENSM-ETVDMPFVKALIQNISTDVSEDLLYSLMLSQIPR 364
Query: 119 QVMKDEDKPPDRVRLPKSLFRSLPGNRSVRLAVTILDIGPGTLFKGPRLGLGDGSGVLN 178
QVM+ ED+P D VRLPKSLF +LPGNRS VRLA+T+LDIG G +FKGP+L GS VLN
Sbjct: 365 QVMQGEDEPADGVRLPKSLFGALPGNRSVRLAITVLDIGAGNVFKGPKLLEDKGSSVLN 544
Query: 179 NRLVGLSVGQMHVTKLAEPLEIVFSHQRPNNMTL 213
NR+VGLSVGQMH T L+EP+EI FSH+R PP M L
Sbjct: 545 NRMVGLSVGQMHATGLSEPVEITFSHERQPPAMIL 649

Score = 84.7 bits (206), Expect(3) = 0.0
Identities = 41/54 (75%), Positives = 45/54 (82%), Gaps = 1/54 (1%)
Frame = +3

Query: 497 PLGLSTVYIFALFNSLQGVFICCWFTILYLPSQSTTVSSS-TARLDQAHSASQE 549
P GLST+Y+F L NSLQG+FI CWF ILY P+QSTT SSS TARLDQAHS SQE
Sbjct: 1599 PPGLSTIYVFLLNSLQGLFIFCWFIIIFYFTQSTTASSSGTARLDQAHSVSQE 1760